

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/511,221
Source: Pg 10
Date Processed by STIC: 10/24/04

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/24/2004

PATENT APPLICATION: US/10/511,221

TIME: 09:52:21

Input Set : A:\LeA36033.ST25.txt

Output Set: N:\CRF4\10242004\J511221.raw

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3 <110> APPLICANT: Bayer CropScience Aktiengesellschaft
5 <120> TITLE OF INVENTION: Helicokinin receptor
7 <130> FILE REFERENCE: Le A 36 033
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,221
C--> 9 <141> CURRENT FILING DATE: 2004-10-13
9 <160> NUMBER OF SEQ ID NOS: 2
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1452
15 <212> TYPE: DNA
16 <213> ORGANISM: Heliothis virescens
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (1)..(1452)
21 <223> OTHER INFORMATION:
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25 atg gac act agt aca aca aat tca tca caa gat gac gac gcg gac tgg      48
26 Met Asp Thr Ser Thr Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp
27 1          5          10          15
29 cca agg aac agt tcc att gac gag tat att ata cac aat gga act aat      96
30 Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn
31          20          25          30
33 gat aca ttc gaa aca ttg tac gat gtg ccg act ggt atg ata gta ctc      144
34 Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu
35          35          40          45
37 ttg tcg ttc ctg tac ggc tca ata tca gtt ctt gcg gtg gtg ggg aac      192
38 Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn
39          50          55          60
41 ttt ctg gtg atg tgg gtc gtg gcc acc tcg aga aga atg cag agc gtc      240
42 Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val
43 65          70          75          80
45 aca aac tgc tac ata gcc aac tta gct tta gct gac ata gtc ata gga      288
46 Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly
47          85          90          95
49 tta ttc gct gta cca ttt caa ttt caa gcc gcg ctg cta cag cgg tgg      336
50 Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp
51          100          105          110
53 ctg cta ccg cac ttc atg tgt ccg ttc tgc ccg ttc gtg cag gcg ctc      384
54 Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu
55          115          120          125
57 agt gtc aac gtc agc gtg ttt aca ctg aca gcc atc gca gtt gac aga      432
58 Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg
59          130          135          140

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61	cat	cgg	gcg	ata	atc	aca	ccg	ctc	agc	gcc	cac	act	tca	aag	cgt	att	480
62	His	Arg	Ala	Ile	Ile	Thr	Pro	Leu	Ser	Ala	His	Thr	Ser	Lys	Arg	Ile	
63	145					150				155					160		
65	gcc	aaa	gta	ata	ata	gtg	gtt	ata	tgg	ttt	ctg	gcg	ctt	tct	tta	gct	528
66	Ala	Lys	Val	Ile	Ile	Val	Val	Ile	Trp	Phe	Leu	Ala	Leu	Ser	Leu	Ala	
67						165				170					175		
69	gct	ccg	atg	gct	atg	tct	tgg	gag	gtt	atc	atg	gaa	gat	gaa	tta	gat	576
70	Ala	Pro	Met	Ala	Met	Ser	Trp	Glu	Val	Ile	Met	Glu	Asp	Glu	Leu	Asp	
71						180				185					190		
73	cca	gtt	gca	aaa	atc	ttc	tac	aaa	aag	ccg	ttt	tgt	gca	ccc	acc	gag	624
74	Pro	Val	Ala	Lys	Ile	Phe	Tyr	Lys	Lys	Pro	Phe	Cys	Ala	Pro	Thr	Glu	
75						195				200					205		
77	ttc	ggc	tcg	cat	tca	ctc	gcc	att	tat	aga	ctg	ttg	ttg	tat	gta	ttt	672
78	Phe	Gly	Ser	His	Ser	Leu	Ala	Ile	Tyr	Arg	Leu	Leu	Leu	Tyr	Val	Phe	
79						210				215					220		
81	cag	tat	gta	atc	ccg	ttg	tgt	gtg	att	acg	ttt	gcc	tac	gct	cat	atg	720
82	Gln	Tyr	Val	Ile	Pro	Leu	Cys	Val	Ile	Thr	Phe	Ala	Tyr	Ala	His	Met	
83	225					230						235				240	
85	gcg	atg	aag	ctg	tgg	gga	gcg	cgc	gcc	cca	ggg	aac	gcg	cag	gag	acg	768
86	Ala	Met	Lys	Leu	Trp	Gly	Ala	Arg	Ala	Pro	Gly	Asn	Ala	Gln	Glu	Thr	
87						245				250					255		
89	agg	gac	gct	aac	cac	atg	cga	aac	aag	aag	aag	gtg	ata	aaa	atg	ttg	816
90	Arg	Asp	Ala	Asn	His	Met	Arg	Asn	Lys	Lys	Lys	Val	Ile	Lys	Met	Leu	
91						260				265					270		
93	gtg	ctg	gtc	gta	gct	ctg	ttt	gcg	tta	tgc	tgg	ctg	ccg	cta	cag	agc	864
94	Val	Leu	Val	Val	Ala	Leu	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Gln	Ser	
95						275				280					285		
97	tac	tta	tta	cta	caa	tca	ttt	ttt	cca	tca	att	aac	gag	tac	aag	tac	912
98	Tyr	Leu	Leu	Leu	Gln	Ser	Phe	Phe	Pro	Ser	Ile	Asn	Glu	Tyr	Lys	Tyr	
99						290				295					300		
101	atc	aac	gtg	ctt	ttc	ttt	tgc	ttc	gac	tgg	cta	gca	atg	agc	aac	tct	960
102	Ile	Asn	Val	Leu	Phe	Phe	Cys	Phe	Asp	Trp	Leu	Ala	Met	Ser	Asn	Ser	
103	305					310						315				320	
105	tgc	tat	aac	cca	ttc	atc	tat	gcc	atc	tac	aac	gaa	aaa	ttc	aag	aag	1008
106	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala	Ile	Tyr	Asn	Glu	Lys	Phe	Lys	Lys	
107						325				330					335		
109	gaa	ttc	aaa	caa	cga	ttc	act	ttc	ggg	aaa	aag	cca	agc	aga	ttc	gtt	1056
110	Glu	Phe	Lys	Gln	Arg	Phe	Thr	Phe	Gly	Lys	Lys	Pro	Ser	Arg	Phe	Val	
111						340				345					350		
113	aac	gat	agc	tac	gag	gac	ggc	cag	tca	tac	cga	aca	aga	att	tta	tcg	1104
114	Asn	Asp	Ser	Tyr	Glu	Asp	Gly	Gln	Ser	Tyr	Arg	Thr	Arg	Ile	Leu	Ser	
115						355				360					365		
117	ttc	cga	tca	acc	aac	gac	aga	agt	ggc	tat	tca	tcc	aga	aag	tct	ttg	1152
118	Phe	Arg	Ser	Thr	Asn	Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Arg	Lys	Ser	Leu	
119						370				375					380		
121	aac	ata	ccg	ccg	ggg	gac	act	tta	aaa	gtt	cct	tct	aga	aat	tca	tgt	1200
122	Asn	Ile	Pro	Pro	Gly	Asp	Thr	Leu	Lys	Val	Pro	Ser	Arg	Asn	Ser	Cys	
123	385					390						395				400	
125	cat	tgc	atg	gcg	aat	cag	agc	aga	gaa	aat	gga	ttt	aac	ttc	atg	aaa	1248

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126 His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys
127          405          410          415
129 act gaa gac atg gaa ggg cac gga aat agc agg cgg tat ctg aat ata      1296
130 Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile
131          420          425          430
133 aga atg agt aat cca gat att ggt aaa aga aga tta gct aag aag tta      1344
134 Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu
135          435          440          445
137 tcg aat aga gac gac atg cct ata ggt gat gag aga gtc agt gaa ctg      1392
138 Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu
139          450          455          460
141 tac ata ttc cca aac agt aac att gta gaa ttt aca gac ata tca tac      1440
142 Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr
143 465          470          475          480
145 gat gac aaa gtg      1452
146 Asp Asp Lys Val
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 484
152 <212> TYPE: PRT
153 <213> ORGANISM: Heliothis virescens
155 <400> SEQUENCE: 2
157 Met Asp Thr Ser Thr Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp
158 1          5          10          15
161 Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn
162          20          25          30
165 Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu
166          35          40          45
169 Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn
170          50          55          60
173 Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val
174 65          70          75          80
177 Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly
178          85          90          95
181 Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp
182          100          105          110
185 Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu
186          115          120          125
189 Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg
190          130          135          140
193 His Arg Ala Ile Ile Thr Pro Leu Ser Ala His Thr Ser Lys Arg Ile
194 145          150          155          160
197 Ala Lys Val Ile Ile Val Val Ile Trp Phe Leu Ala Leu Ser Leu Ala
198          165          170          175
201 Ala Pro Met Ala Met Ser Trp Glu Val Ile Met Glu Asp Glu Leu Asp
202          180          185          190
205 Pro Val Ala Lys Ile Phe Tyr Lys Lys Pro Phe Cys Ala Pro Thr Glu
206          195          200          205
209 Phe Gly Ser His Ser Leu Ala Ile Tyr Arg Leu Leu Leu Tyr Val Phe
210          210          215          220

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```

213 Gln Tyr Val Ile Pro Leu Cys Val Ile Thr Phe Ala Tyr Ala His Met
214 225                230                235                240
217 Ala Met Lys Leu Trp Gly Ala Arg Ala Pro Gly Asn Ala Gln Glu Thr
218                245                250                255
221 Arg Asp Ala Asn His Met Arg Asn Lys Lys Lys Val Ile Lys Met Leu
222                260                265                270
225 Val Leu Val Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Leu Gln Ser
226                275                280                285
229 Tyr Leu Leu Leu Gln Ser Phe Phe Pro Ser Ile Asn Glu Tyr Lys Tyr
230                290                295                300
233 Ile Asn Val Leu Phe Phe Cys Phe Asp Trp Leu Ala Met Ser Asn Ser
234 305                310                315                320
237 Cys Tyr Asn Pro Phe Ile Tyr Ala Ile Tyr Asn Glu Lys Phe Lys Lys
238                325                330                335
241 Glu Phe Lys Gln Arg Phe Thr Phe Gly Lys Lys Pro Ser Arg Phe Val
242                340                345                350
245 Asn Asp Ser Tyr Glu Asp Gly Gln Ser Tyr Arg Thr Arg Ile Leu Ser
246                355                360                365
249 Phe Arg Ser Thr Asn Asp Arg Ser Gly Tyr Ser Ser Arg Lys Ser Leu
250                370                375                380
253 Asn Ile Pro Pro Gly Asp Thr Leu Lys Val Pro Ser Arg Asn Ser Cys
254 385                390                395                400
257 His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys
258                405                410                415
261 Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile
262                420                425                430
265 Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu
266                435                440                445
269 Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu
270                450                455                460
273 Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr
274 465                470                475                480
277 Asp Asp Lys Val

```

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21